

MRLEGPGLSLLCLVLALPALLPVPVAVRGVAETPTYPRDAETGERLVCAQCPPGTFVQR
PCRRDSPITCGPCPPRHYTQFWNYLERCRYCNVLCGEREEEARACHATHNRACRCRTGFF
AHAGFCLEHASCPPGAGVIAPGTFSQNTQCPCPPGTFSASSSSSEQQPHRNCTALGLA
LNVPGSSSHDTLCTSGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQALEAPE
GWGPTPRAGRAALQLKLRRLTELLGAQDGALLVRLLQALRVARMPGLERSVRERFLPVH

Fig. 1

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 GCAGAGACAGGGGAGCGGCTGGTGTGCGCCCACTGCCCCCAGGCACCTTTGTGCAGCGG
 CCGTGCCGCGGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
 TTCTGGAACTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
 GAGGCACGGGCTTGCCACGCCACCCACAACCGTGCTGCCGCTGCCGCACCGGCTTCTTC
 GCGCACGCTGGTTTCTGCTTGAGCAGCATCGTGTCCACCTGGTGCCGGCGTGATTGCC
 CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCC
 AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
 CTCAATGTGCCAGGCTCTTCTCCCATGACACCCCTGTGCACCAGCTGCACTGGCTTCCCC
 CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
 TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCGGAG
 GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCTTGCAGCTGAAGCTGCGTCGGCGG
 CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGCGGCTGCTGCAGGCGCTG
 CGCGTGGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCCTGTGCAC
 TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCCACTTGCCTGAAAGAGG
 CTTTTTTTTTAAATAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

Fig. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAAGTGGAGCNCTGCCGCTACTGNAACGTCTCTGNNG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCAT

Fig. 3

SEQ ID NO: 4 128 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 5 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 SEQ ID NO: 6 1
 SEQ ID NO: 3 1 GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
 G
 SEQ ID NO: 4 178 CA-TTCTGGAACCTCGAGCGC
 SEQ ID NO: 5 51 CAGTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
 SEQ ID NO: 6 2 CAGTCTGGAACCTCGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
 SEQ ID NO: 3 51 CAGTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNGG
 SEQ ID NO: 5 101 GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGGCCT
 SEQ ID NO: 6 52 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
 SEQ ID NO: 7 1 GAGGGCCCCCAGGAGTGGTGGCGGAGGTG
 SEQ ID NO: 3 101 GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
 SEQ ID NO: 5 151 GCNGCTGCAGCACCCGGNTTCTTCGCGCACGCTGNTTCTGCTTGGAGCAC
 SEQ ID NO: 6 102 GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
 SEQ ID NO: 7 32 TGGCAGGGGTACAGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACAC
 SEQ ID NO: 3 151 GCCGCTGCCGCACCCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGGAGCAC
 SEQ ID NO: 5 201 GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
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 SEQ ID NO: 7 82 CAGTTCCCTGACCCCTGTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
 SEQ ID NO: 8 1 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCGGGCACCCCCAGCCA
 SEQ ID NO: 10 1 CTTGTCCACCTGGTGCCGGCGTGATTNCCC-GGGCACCCCCAGCCA
 SEQ ID NO: 3 201 GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCGGGCACCCCCAGCCA

Fig. 4

SEQ ID NO: 5 251 GAACACGCA-TGCAAAAGCCGTG
 SEQ ID NO: 7 132 GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 8 51 GAACACGCAG-GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 10 47 GAACACGCAGTCCC-AGCCNT-CCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 9 1 AGCNGTGCCNCCNAGGCACCTTCTCAGCCAGCAGT
 SEQ ID NO: 3 251 GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
 SEQ ID NO: 7 182 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT
 SEQ ID NO: 8 101 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT
 SEQ ID NO: 10 97 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGNC-T
 SEQ ID NO: 9 36 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT
 SEQ ID NO: 3 301 TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCCCTGGGCCT
 SEQ ID NO: 7 232 GGCCCTCAATGTGCCAGGCTCTTCTCTCCATGACACCCCTGTGCACCAG
 SEQ ID NO: 8 151 GGCCCTCAATGTGCCAGGCTCTTCTCTCCATGACACCCCTGTGCACCAGCT
 SEQ ID NO: 10 147 GGCCCTCAATGTGCCAGGCTCTTCTCTCCATGACACCCCTGTGCACCAGCT
 SEQ ID NO: 9 86 GGCCCTCAATGTGCCAGGCTCTTCTCTCCATGACACCCCTGTGCACCAGCT
 SEQ ID NO: 3 351 GGCCCTCAATGTGCCAGGCTCTTCTCTCCATGACACCCCTGTGCACCAGCT
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 SEQ ID NO: 9 136 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 3 401 GCACTGGCTTCCCCCTCAGCACCCAGGTACCAGGAGCTGAGGAGTGTGAG
 SEQ ID NO: 10 247 CGTGCCGTTCATCGACTTTGTGGCTTTCAGGACATCTCCAT
 SEQ ID NO: 9 186 CGTGCCGTTCATCGACTTTGTGGCTTTCAGGACATCTCCAT
 SEQ ID NO: 3 451 CGTGCCGTTCATCGACTTTGTGGCTTTCAGGACATCTCCAT

Fig. 4 (cont.)

UNA 30942
H1NFR2

1 MRALEGGFGLSLLCEVIALPAALLPVPVAVRGVAIIPITYPWFD AEIG
1 MAPVAVWALAVGLLWAAAHALPAQVAFIPY APLDGSICRLRETYDQI

UNA 30942
H1NFR2

CRD1 CRD2

15 ERLVCAQCPRPGTFVQRPCCRDSPTTCGP C PPRHYIQFWHYLERCRYGNVL
50 AQMCCKSKCSPGQNAKVFCXTXSDIVCDSCEOSTYTQLWNWVPECISCGSR

UNA 30942
H1NFR2

CRD2 CRD3

75 CGEREEEARACHATHNRACRCRTGFF...AAAG...FLEHASCP PGAGV
100 CSSDQVETQACTREDNRICTCRPGWYCALSKEGCRLCAPLRKCRPGFGV

UNA 30942
H1NFR2

CRD3 CRD4

139 IAPGTFSQNTQCQPCPGTFSASSSSSEQCOPHRNCTALGLALMVPGSSS
150 ARPGETETSDVCKPCAPGTFSNTTSSSTDICRPHQICWVVA...IPGNAS

UNA 30942
H1NFR2

CRD4

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196 RDAVCTSTST...PTRSMAPGAVHLPQVSTRSQHTQPTPEPSTAPSTSFLL

UNA 30942
H1NFR2

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244 PMGSPSPAEGSTGDFALPYGLIVGVIALGLLLIGVVHCVIMTQVKKKPL

UNA 30942
H1NFR2

287 GLERSYRERFLPVH
293 CLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSASALORRA

H1NFR2

343 PTRNOPQAPGVEASGAGEARASTGSSDSSPGGHGTQVNVTCIVNVCSSSD

H1NFR2

393 HSSQCSSQASSTMGDTDSSSPSES PKDEQVPFSKEECAFRSOLETPETLLG

H1NFR2

443 STEEKPLPLGVDPDAGMKPS

Fig. 5

DcR3 1 M R A L E G P G L S L L C L V L A L P A L L P V P A V R G V A 31
 OPG 1 M N K L L C C A L V F L D I S I K W T T Q E T F P 25

CRD1
 DcR3 32 E T P T Y P W R D A E T G E R L V C A Q C P P G T F V Q R P C 62
 OPG 26 . . P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T T C G P C P P R H Y T Q F W N Y L E R C R Y C N V 93
 OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

CRD2
 DcR3 94 L C G E R E E E A R A C H A T H N R A C R C R T G F F A H A G 124
 OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

CRD3
 DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
 OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

CRD4
 DcR3 156 G T F S A S S S S S E Q C Q P H R N C T A L G L A L N V P G S 186
 OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
 OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
 OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
 OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
 OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

Fig. 6

100%
 80%
 60%
 40%
 20%
 0%

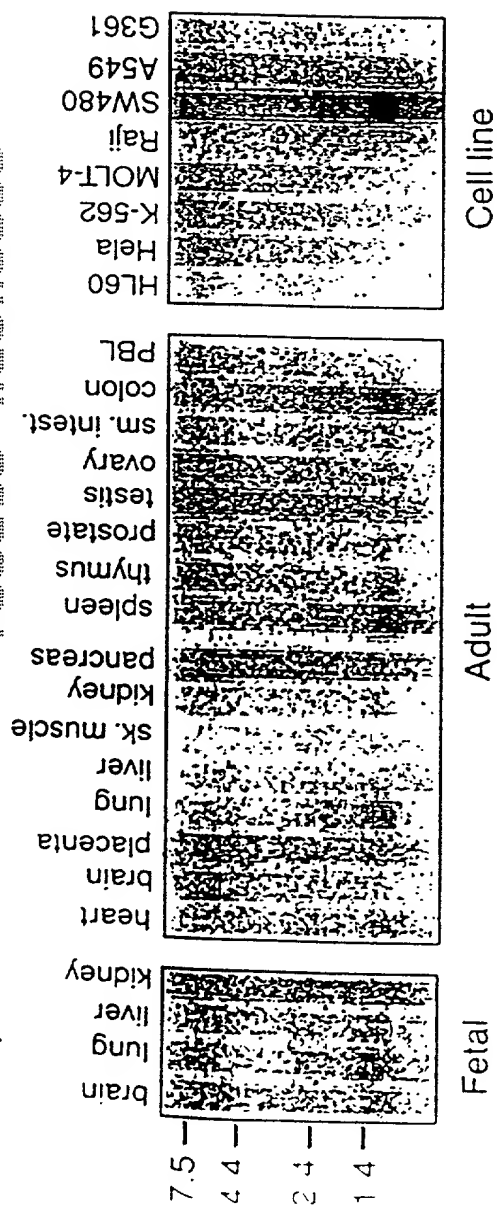


Fig. 7

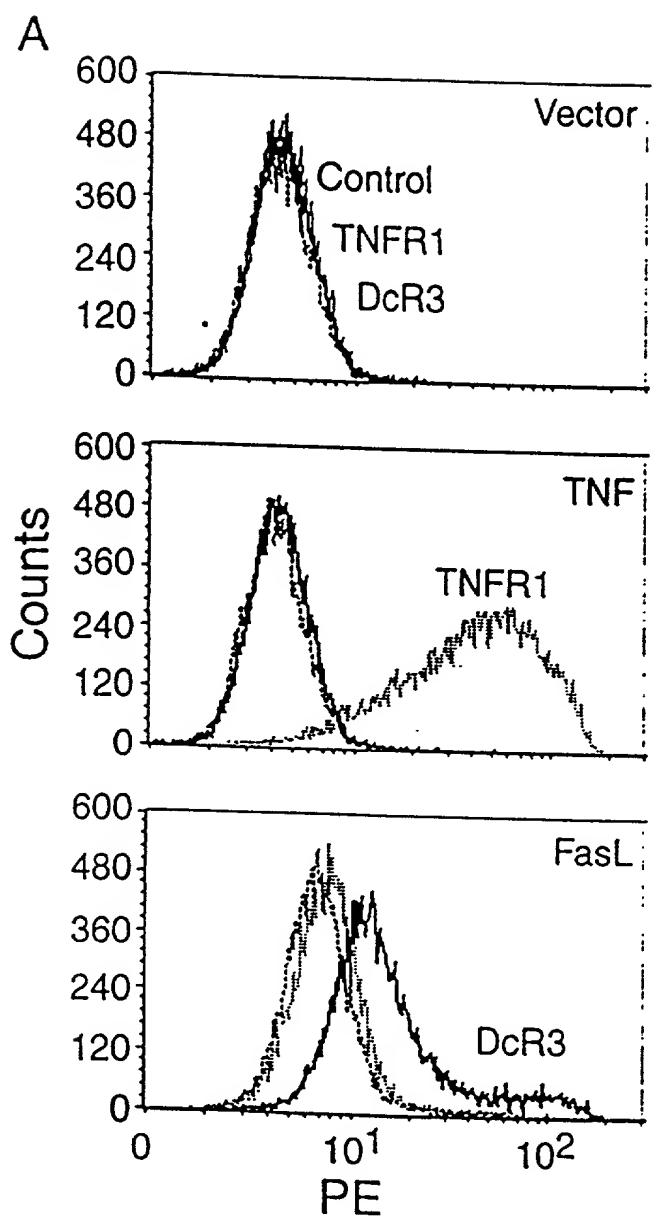
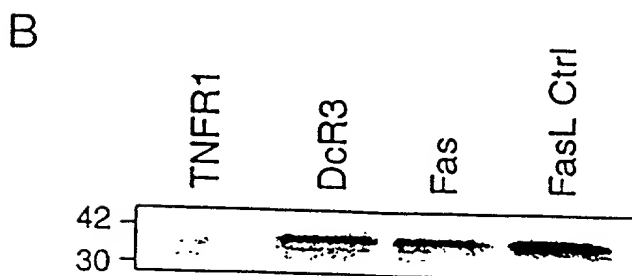


Fig. 8



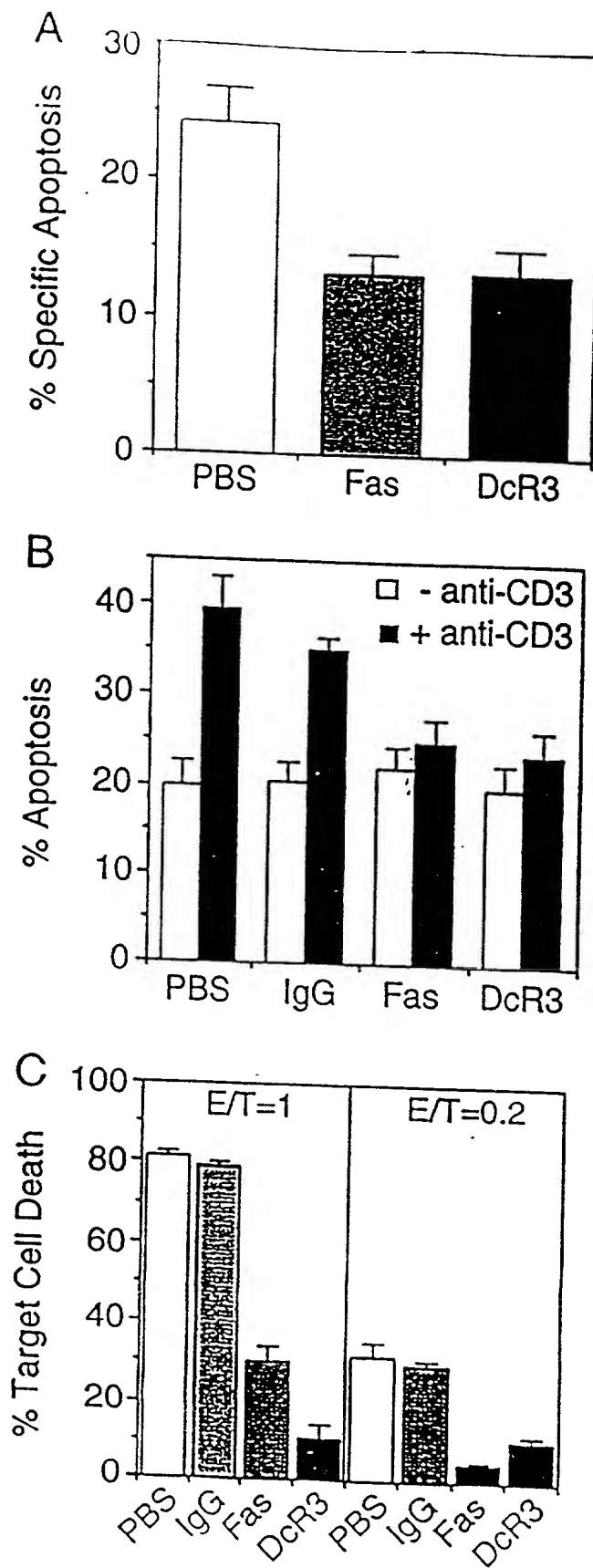


Fig. 9

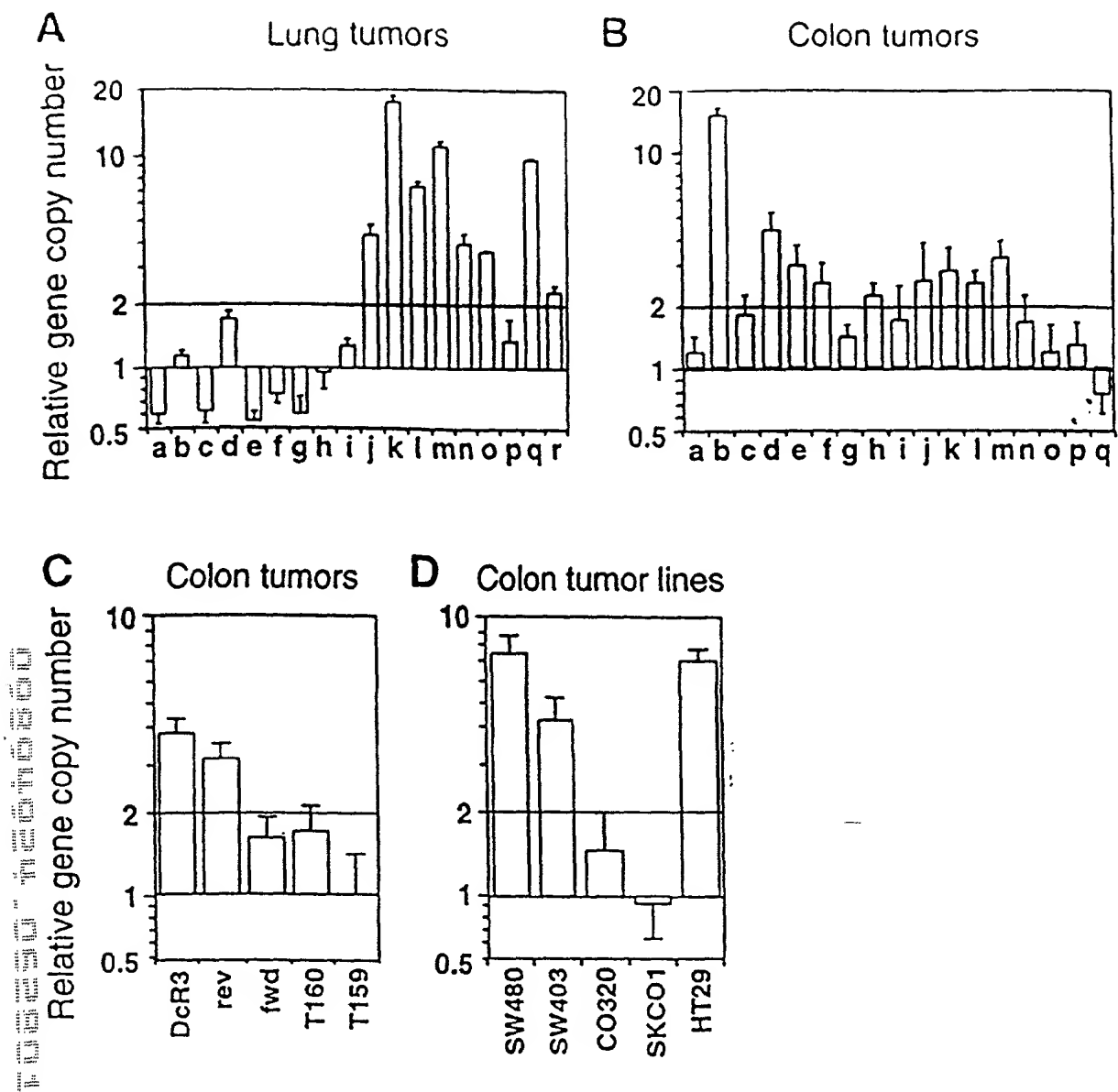


Fig. 10

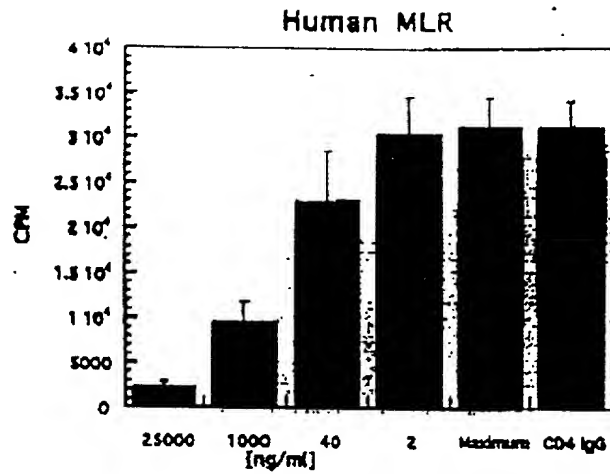


Fig. 11A

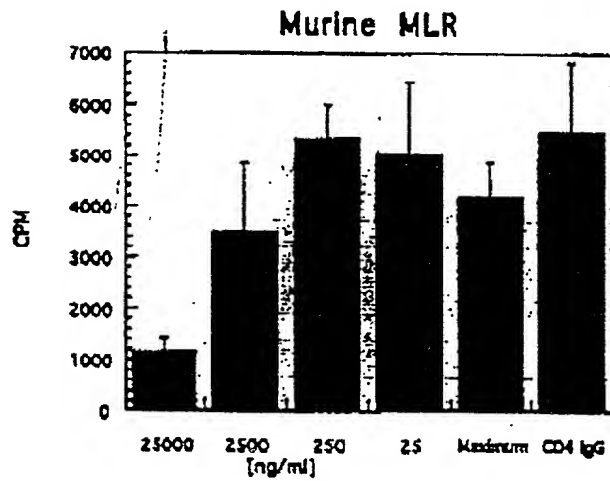


Fig. 11B

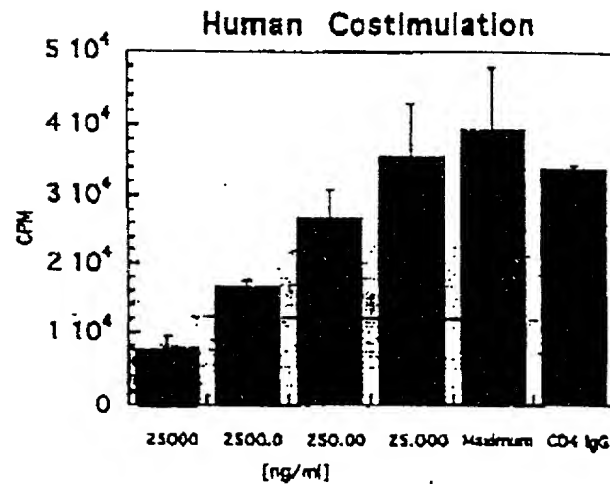


Fig. 11C

Variable	Mean	Standard deviation	Minimum	Maximum	Skewness	Kurtosis	Jarque-Bera	Probability
Return	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Volatility	0.0100	0.0050	0.0000	0.0200	0.0000	3.0000	0.2264	0.8841
Information	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Market	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Size	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Book-to-market	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Dividend yield	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Turnover	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Age	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Industry	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Country	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Market cap	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Debt to equity	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Profit margin	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Return on assets	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Return on equity	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Operating margin	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Capital expenditures	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Research and development	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Advertising	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
SG&A	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Interest expense	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Income tax expense	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Depreciation	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Amortization	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Goodwill	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Intangible assets	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Net income	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Operating income	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Pre-tax income	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Net operating assets	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Operating assets	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Non-operating assets	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Operating liabilities	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Non-operating liabilities	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841
Operating income per share	0.0000	0.0100	-0.0200	0.0200	0.0000	3.0000	0.2264	0.8841

Antigen specificity was determined using 10 microgram/ml mAb.
 * blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

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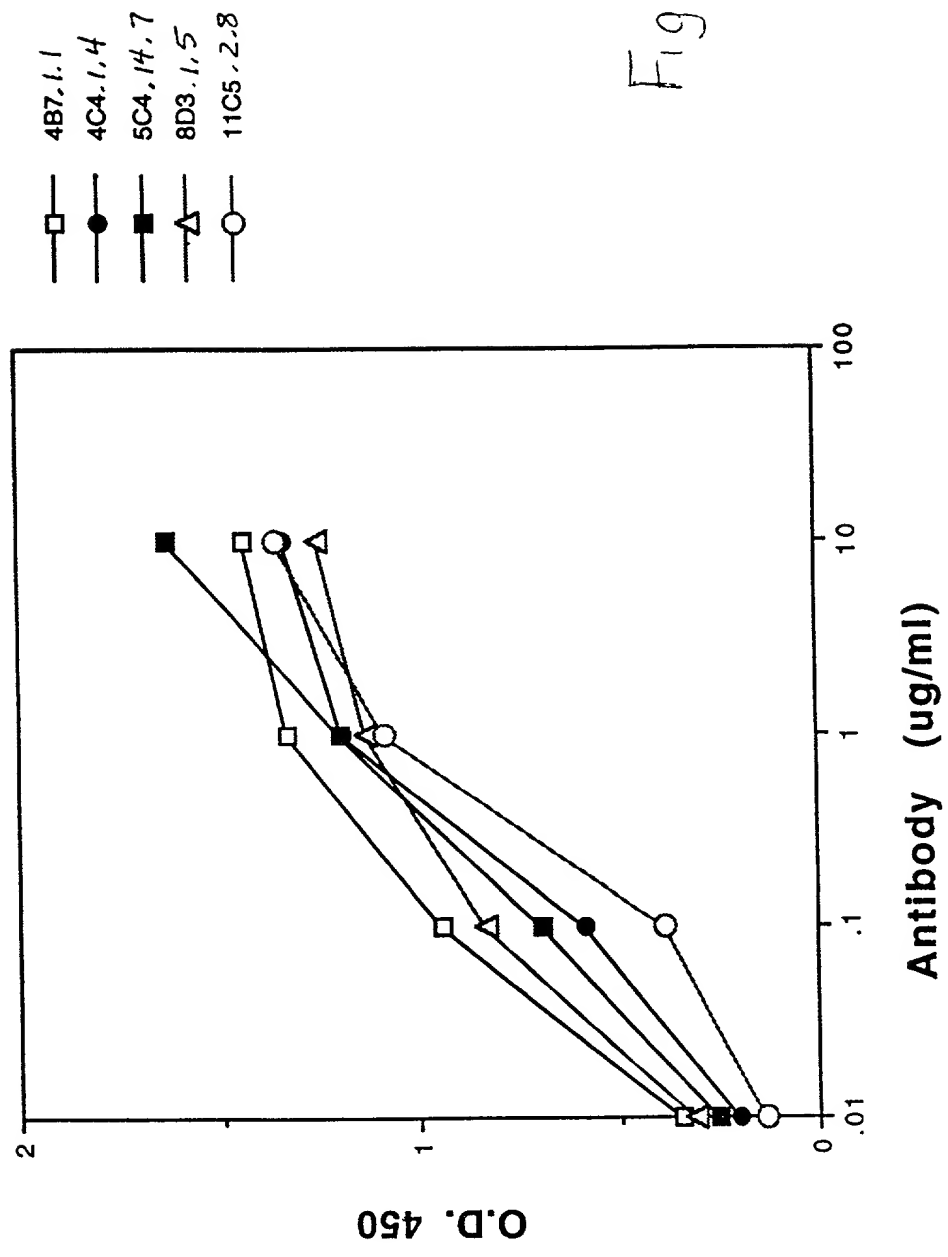


Fig. 13

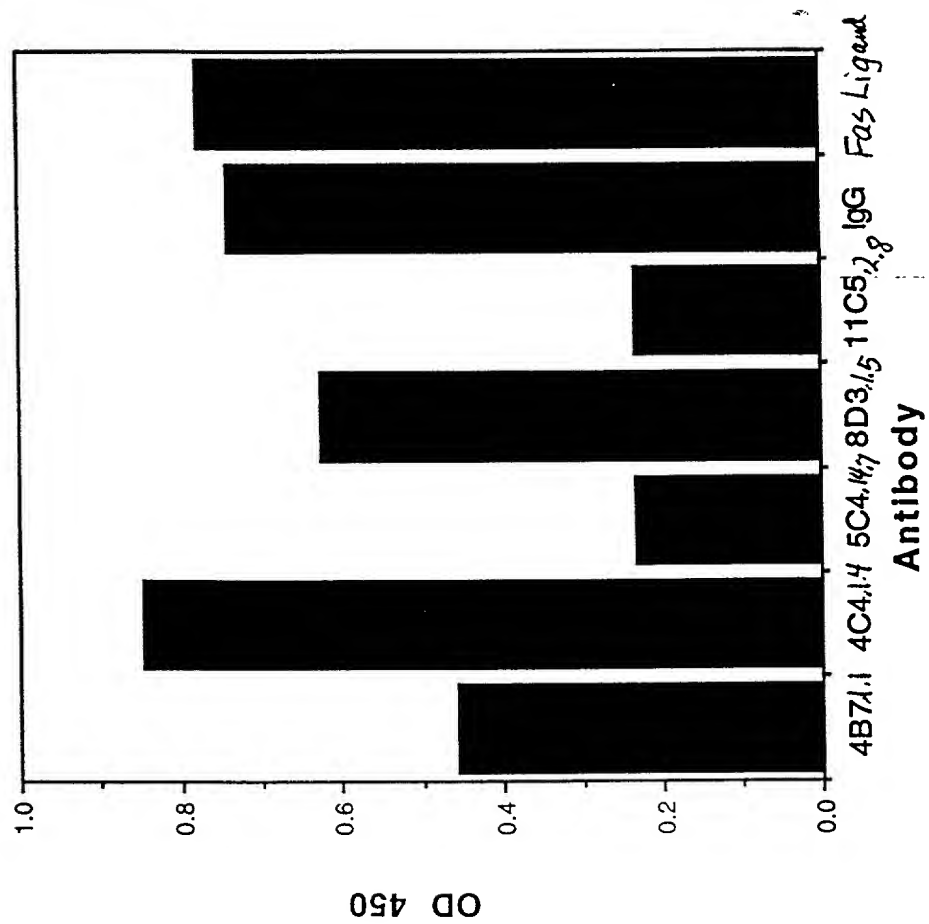


Fig. 14